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**RAW SEQUENCE LISTING
PATENT APPLICATION US/08/887,977**

SECTOR

DATE: 03/09/98

TIME: 14:52:15 4/20/98

INPUT SET: S24076.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Wang, Wei
Gish, Kurt C.
Schall, Thomas J.
Vicari, Alain P.
Zlotnik, Albert

11 (ii) TITLE OF INVENTION: MAMMALIAN CHEMOKINE REAGENTS

13 (iii) NUMBER OF SEQUENCES: 19

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: DNAX Rese...
17 (B) STREET: 901 Californ...
18 (C) CITY: Palo Alto
19 (D) STATE: California
20 (E) COUNTRY: USA
21 (F) ZIP: 94304-1104

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

30 (A) APPLICATION NUMBER: US 08/887,977
31 (B) FILING DATE: 03-JUL-1997
32 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER: US 60/021,644
36 (B) FILING DATE: 05-JUL-1996

38 (vii) PRIOR APPLICATION DATA:

39 (A) APPLICATION NUMBER: US 60/028,329
40 (B) FILING DATE: 11-OCT-1996

42 (viii) ATTORNEY/AGENT INFORMATION:

43 (A) NAME: Ching, Edwin P.
44 (B) REGISTRATION NUMBER: 34,090
45 (C) REFERENCE/DOCKET NUMBER: DX0589K1

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47 (ix) TELECOMMUNICATION INFORMATION:
48 (A) TELEPHONE: 650-852-9192
49 (B) TELEFAX: 650-496-1200

50

51

52 (2) INFORMATION FOR SEQ ID NO:1:

53

54 (i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 1034 base pairs
56 (B) TYPE: nucleic acid
57 (C) STRANDEDNESS: single
58 (D) TOPOLOGY: linear

59

60 (ii) MOLECULE TYPE: cDNA

61

62

63 (ix) FEATURE:
64 (A) NAME/KEY: CDS
65 (B) LOCATION: 94..525

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68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

69

70 AGGCTACAAG CAGGCACCAAG CTCTCAGGAC CAGAAAGGCA TTGGTGGCCC CCTTAAACCT 60

71

72 TCAGGTATCT GGAGAGGAGA TCTAACCTTC ACT ATG AAA CTG TGG CTT TTT GCC 114
Met Lys Leu Trp Leu Phe Ala
73 1 5

74

75 TGC CTG GTT GCC TGT TTT GTT GGG GCC TGG ATG CCG GTT GTC CAT GCC 162
Cys Leu Val Ala Cys Phe Val Gly Ala Trp Met Pro Val Val His Ala
76 10 15 20

77

78 CAA GGT GCC TTT GAA GAC TGC TGC CTG GGT TAC CAG CAC AGG ATC AAA 210
Gln Gly Ala Phe Glu Asp Cys Cys Leu Gly Tyr Gln His Arg Ile Lys
79 25 30 35

80 TGG AAT GTT CTC CGG CAT GCT AGG AAT TAT CAC CAG CAG GAA GTG AGT 258
Trp Asn Val Leu Arg His Ala Arg Asn Tyr His Gln Gln Glu Val Ser
81 40 45 50 55

82 GGA AGC TGC AAC CTA CGT GCT GTG AGA TTC TAC TTC CGC CAG AAA GTA 306
Gly Ser Cys Asn Leu Arg Ala Val Arg Phe Tyr Phe Arg Gln Lys Val
83 60 65 70

84

85 GTG TGT GGG AAT CCA GAG GAC ATG AAT GTG AAG AGG GCG ATA AGA ATC 354
Val Cys Gly Asn Pro Glu Asp Met Asn Val Lys Arg Ala Ile Arg Ile
86 75 80 85

87

88 TTG ACA GCT AGG AAA AGG CTA GTC CAC TGG AAG AGC GCC TCA GAC TCT 402
Leu Thr Ala Arg Lys Arg Leu Val His Trp Lys Ser Ala Ser Asp Ser
89 90 95 100

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PATENT APPLICATION US/08/887,977DATE: 03/09/98
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100	CAG ACT GAA AGG AAG AAC CAT ATG AAG TCC AAG GTG GAG AAC	450
101	Gln Thr Glu Arg Lys Lys Ser Asn His Met Lys Ser Lys Val Glu Asn	
102	105 110 115	
103		
104	CCC AAC AGT ACA AGC GTG AGG AGT GCC ACC CTA GGT CAT CCC AGG ATG	498
105	Pro Asn Ser Thr Ser Val Arg Ser Ala Thr Leu Gly His Pro Arg Met	
106	120 125 130 135	
107		
108	GTC ATG ATG CCC AGA AAG ACC AAC AAT TAAGTTAATT ACTCAGAGTA	545
109	Val Met Met Pro Arg Lys Thr Asn Asn	
110	140	
111		
112	AGCACCCAGCT GGAGGATGGG CGGAGTCTGC TGAAGTGCTG TCTTCTAGGC ATGCCAGTGC	605
113		
114	CAATGAACTC ACTGAAGCTA CAGTTTCCTG TACAAGACCA GACCCACCAA CGTCTCAGCA	665
115		
116	TGTACGAGGA AGGAACTACT GCGCTAAAGG CCCTCCCACT CACCAAGGAG CTATTGGCTA	725
117		
118	TTGATGATTG CTGAGGGAAAG GGAGTAATT TTTTCTCTT TCTGAAGTGT GACTTGAGTA	785
119		
120	AATTGCCCAT AGTCAGTAT ATAATCCCCA ACCTGTGCTC AGGCAAGCAA CCCTAATTAA	845
121		
122	ATGCAATAGC CACATACAAA AGAAGAGGAT ATGAATAGTT TGGTAGGAGG GGCTTGTAG	905
123		
124	GAAGAAGACA TTAACAGGAG AGAGAGGAGC GAGAGGATAG TGAGTGTGTG AGAGTGCCTG	965
125		
126	CACGTGTGAA ATGGTCAAAG AATTAACCTTA AAAAGCTATT AAAAAGTAAA	1025
127		
128	AAAAATAAA	1034
129		
130		
131	(2) INFORMATION FOR SEQ ID NO:2:	
132		
133	(i) SEQUENCE CHARACTERISTICS:	
134	(A) LENGTH: 144 amino acids	
135	(B) TYPE: amino acid	
136	(D) TOPOLOGY: linear	
137		
138	(ii) MOLECULE TYPE: protein	
139		
140	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
141		
142	Met Lys Leu Trp Leu Phe Ala Cys Leu Val Ala Cys Phe Val Gly Ala	
143	1 5 10 15	
144		
145	Trp Met Pro Val Val His Ala Gln Gly Ala Phe Glu Asp Cys Cys Leu	
146	20 25 30	
147		
148	Gly Tyr Gln His Arg Ile Lys Trp Asn Val Leu Arg His Ala Arg Asn	
149	35 40 45	
150		
151	Tyr His Gln Gln Glu Val Ser Gly Ser Cys Asn Leu Arg Ala Val Arg	
152	50 55 60	

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153
154 Phe Tyr Phe Arg Gln Lys Val Val Cys Gly Asn Pro Glu Asp Met Asn
155 65 70 75 80
156
157 Val Lys Arg Ala Ile Arg Ile Leu Thr Ala Arg Lys Arg Leu Val His
158 85 90 95
159
160 Trp Lys Ser Ala Ser Asp Ser Gln Thr Glu Arg Lys Lys Ser Asn His
161 100 105 110
162
163 Met Lys Ser Lys Val Glu Asn Pro Asn Ser Thr Ser Val Arg Ser Ala
164 115 120 125
165
166 Thr Leu Gly His Pro Arg Met Val Met Met Pro Arg Lys Thr Asn Asn
167 130 135 140
168
169
170 (2) INFORMATION FOR SEQ ID NO:3:
171
172 (i) SEQUENCE CHARACTERISTICS:
173 (A) LENGTH: 1012 base pairs
174 (B) TYPE: nucleic acid
175 (C) STRANDEDNESS: single
176 (D) TOPOLOGY: linear
177
178 (ii) MOLECULE TYPE: cDNA
179
180
181 (ix) FEATURE:
182 (A) NAME/KEY: CDS
183 (B) LOCATION: 117..566
184
185 (ix) FEATURE:
186 (A) NAME/KEY: mat_peptide
187 (B) LOCATION: 186..566
188
189
190 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
191
192 TCGACCCACG CGTCCGCTTG GCCTACAGCC CGGCGGGCAT CAGCTCCCTT GACCCAGTGG 60
193
194 ATATCGGTGG CCCC GTTATT CGTCCAGGTG CCCAGGGAGG AGGACCCGCC TGCAGC 116
195
196 ATG AAC CTG TGG CTC CTG GCC TGC CTG GTG GCC GGC TTC CTG GGA GCC 164
197 Met Asn Leu Trp Leu Leu Ala Cys Leu Val Ala Gly Phe Leu Gly Ala
198 -23 -20 -15 -10
199
200 TGG GCC CCC GCT GTC CAC ACC CAA GGT GTC TTT GAG GAC TGC TGC CTG 212
201 Trp Ala Pro Ala Val His Thr Gln Gly Val Phe Glu Asp Cys Cys Leu
202 -5 1 5
203
204 GCC TAC CAC TAC CCC ATT GGG TGG GCT GTG CTC CGG CGC GCC TGG ACT 260
205 Ala Tyr His Tyr Pro Ile Gly Trp Ala Val Leu Arg Arg Ala Trp Thr

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206	10	15	20	25	
207					
208	TAC CGG ATC CAG GAG GTG AGC GGG AGC TGC AAT CTG CCT GCT GCG ATA				308
209	Tyr Arg Ile Gln Glu Val Ser Gly Ser Cys Asn Leu Pro Ala Ala Ile				
210	30	35		40	
211					
212	TTC TAC CTC CCC AAG AGA CAC AGG AAG GTG TGT GGG AAC CCC AAA AGC				356
213	Phe Tyr Leu Pro Lys Arg His Arg Lys Val Cys Gly Asn Pro Lys Ser				
214	45	50		55	
215					
216	AGG GAG GTG CAG AGA GCC ATG AAG CTC CTG GAT GCT CGA AAT AAG GTT				404
217	Arg Glu Val Gln Arg Ala Met Lys Leu Leu Asp Ala Arg Asn Lys Val				
218	60	65		70	
219					
220	TTT GCA AAG CTC CAC AAC ATG CAG ACC TTC CAA GCA GGC CCT CAT				452
221	Phe Ala Lys Leu His His Asn Met Gln Thr Phe Gln Ala Gly Pro His				
222	75	80		85	
223					
224	GCT GTA AAG AAG TTG AGT TCT GGA AAC TCC AAG TTA TCA TCA TCC AAG				500
225	Ala Val Lys Lys Leu Ser Ser Gly Asn Ser Lys Leu Ser Ser Ser Lys				
226	90	95		100	105
227					
228	TTT AGC AAT CCC ATC AGC AGC AAG AGG AAT GTC TCC CTC CTG ATA				548
229	Phe Ser Asn Pro Ile Ser Ser Lys Arg Asn Val Ser Leu Leu Ile				
230	110	115		120	
231					
232	TCA GCT AAT TCA GGA CTG TGAGCCGGCT CATTCTGGG CTCCATCGC				596
233	Ser Ala Asn Ser Gly Leu				
234	125				
235					
236	ACAGGAGGGG CCGGATCTT CTCCGATAAA ACCGTCGCCC TACAGACCCA GCTGTCCCCA				656
237					
238	CGCCTCTGTC TTTGGGTCA AGTCTTAATC CCTGCACCTG AGTTGGTCCT CCCTCTGCAC				716
239					
240	CCCCACCAACC TCCTGCCCGT CTGGCAACTG GAAAGAAGGA GTTGGCCTGA TTTAACCTT				776
241					
242	TTGCCGCTCC GGGGAACAGC ACAATCCTGG GCAGCCAGTG GCTCTTGTAG AGAAAACCTTA				836
243					
244	GGATACCTCT CTCACTTCT GTTTCTTGCC GTCCACCCCG GGCCATGCCA GTGTGTCTC				896
245					
246	TGGGTCCCCCT CCAAAATCT GGTCAATTCAA GGATCCCCCTC CCAAGGCTAT GCTTTCTAT				956
247					
248	AACTTTAAA TAAACCTTGG GGGGTGAATG GAATAAAAAA AAAAAAAA AAAAAA				1012
249					
250					
251	(2) INFORMATION FOR SEQ ID NO:4:				
252					
253	(i) SEQUENCE CHARACTERISTICS:				
254	(A) LENGTH: 150 amino acids				
255	(B) TYPE: amino acid				
256	(D) TOPOLOGY: linear				
257					
258	(ii) MOLECULE TYPE: protein				

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION **US/08/887,977**

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Original Text